

# Structure of HTPL and alignment of Patched motifs.

**FIG. 1A**

HTPL-L (954 a.a.)



HTPL-S (767 a.a.)



**FIG. 1B**

Patched motif

Patched

Patched motif		10	20	30	40	50	60	70	80
		..... .....*..... .....*..... .....*..... .....*..... .....*..... .....*..... .....*.....							
consensus	1	VLSSKIRYTF	TPDDIRSYTERGSRSEHEPL	-VERKFFPGDGYPISRFSII	TAKARNS-NILDIRYLN	EVVQVND	FISTNV	78	
HTPL-L	162	deeedleehy	TPVGS	PAKAERRFVQGHFT	TnDSYRFSASRRSTEANFVSL	LVVSYSD-SLLDPAT	FAEVSKLDGAVQDLR	240	
gi 1825729	47	NPLSDAVYL	FTPLGAQSKMERMS	IHEKWPL-TDNNYIP	GRAVTQ	SREIQVTALARND	SNILDPKFANAVYQLDKYIQTRV	125	
gi 1707052	22	NVYSLLMIFGPY	--SYTERRIIHDAWPL	-VDGTFVAGRAVTQ	SREVQVAVVARSGG	NILDRVFSNELKLMESFIRNNI	97		
gi 3892144	49	LRVDDPSYV	FTPSDARWRREISVFENENWPL	-DENKFLPGKSFEAKRFVNILIRAKDGG	SIMRDNVLHEIEILNQWIMNNI	127			
		90	100	110	120	130	140	150	160
		.....*..... .....*..... .....*..... .....*..... .....*..... .....*..... .....*..... .....*.....							
consensus	79	TIPVSG--	ITLSFKDLCMR	FCDINCPVNQHYNGQILRSNLHNSRID	LTYP	TMTFFG	TKIYLGPNFGG	VKLDPN--	PGN- 152
HTPL-L	241	VAREKG--	SQIQYQQVCARYAL	CVPPNPILYAWQV	NKTNLS--SISFPAYNEGRHPL	YLTGFFGGYILGGS--	LGMG	313	
gi 1825729	126	RVLHNG--	HYYSYKNLCLQYKNGGCPSNKHV	--HILSDLHNHGFNITYPYFRF	SGEGYIGSSLGGVTVMKgenetDI-	199			
gi 1707052	98	TVQFSN--	RTWSFADLCLAGp	DCRCANNNDHI---QLASRLHQHG	INITYPTVRLSDKSAYIASALGGV	KLAKgdngeNI-	171		
gi 3892144	128	SIPTDDlk	FNLTYQDLCLSY-DWVCCGANEHIQ	-MLLRNDVNQILD	LHFPRGGTKDTPVYLG	GIFG	VDVQFFQn----	GT- 200	

## FIG. 1B

### Patched motif (Continued)

	170	180	190	200	210	220	230	240	
	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	
consensus	153	--IKSVKAI	VYRLKRD	PEEVEDS	KEWEL	SDFYLE	NEYASD	-HIQ-VT	FSDQVLED--ELVRNGLT
HTPL-L	314	qLLRAKAM	RLLYL	KTDE	PEYDVQ	SKQWL	THLLDQ	TNKNIL-AL	KKIEVVHFTSLSRqlE
gi	1825729	200	--LASAKA	WFMIYH	LKFHPE	MSYISG	EWELGR	MLTQY	PEDP-YIS-ITYFHSQ
gi	1707052	172	--IVEATA	WLLIYQ	LKFYPN	EISYV	SGLW	EREFKN	MDYKKQAKYIS-ITYFHSQ
gi	3892144	201	--LSDAKL	TQLFYF	LKQDQK	QKMWEE	YSKFSY	ALETFL	NQVYSSD-VIT-LSFAHYQ
	250	260	270	280	290	300	310	320	
	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	
consensus	227	ILVTF	SILTSV	RLAS-G	SLHIDW	VRSKP	ILAILG	VLTPL	MAIVSAFGLLFWL
HTPL-L	393	LIILFA	VTSC	FRF----	DCIRN	KMCVA	AFGVI	SAFLA	WVGFGLLHIGV
gi	1825729	274	LLIVF	STLCS	LFD-G	SFIDW	LSKP	ILSIL	GVVSAGIAIL
gi	1707052	247	ILVCF	SVLCS	IVTIK-G	SGYIDW	VVTKP	ILSVL	GVSNAGMGI
gi	3892144	275	VLAMYA	LVSSFT	LKSSAT	KIDWIS	SKPWL	AAAGM	FSTVLISIAF
	330	340	350	360	370	380	390	400	
	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	
consensus	294	---AIGV	DDMFL	MVHAWQ	TRTS	LSVKKR	MGEV	LEEAG	PSITITSL
HTPL-L	453	---GVG	VDDMF	IMISAW	HKTNL	AGDIR	ERM	SNVSKA	AVSITIT
gi	1825729	341	---AVG	VDNMFL	MVAAR	RTSR	THV	HERM	GEC
gi	1707052	314	---AVG	TDNMFL	MVASL	KRTDR	NLKYD	QRIAE	CMADA
gi	3892144	355	qipA	IGIDDM	FLMNAC	WDQTS	KSLSV	PERMSK	TLSHAG
	410	420	430	440	450	460	470	480	
	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	..... .....*	
consensus	371	QLTFF	FAAIMA	IAGK	YEMK	GRHSL	FLR---	AVDA	AETESP---
HTPL-L	530	NITCF	GAFMAL	DGKR---	VVCL	W----	LKKAD	PKWPS---	FKKFC
gi	1825729	418	QITFF	AAACLA	LAMK	HEASGR	NSLFlie---	AVSA	EKKTS
gi	1707052	391	QLTFF	CAILV	YTRI	EEQGLH	SIWLRp---	AVT	YSST
gi	3892144	435	QLTFF	SGAM	AIMGE	VEREK	RHCLFF	YrtfqL	VDISK

FIG. 1

## FIG. 1B

### Patched motif (Continued)

	490	500	510	520	530	540	550	560	
consensus	417	..... .....*..... .....*..... .....*..... .....*..... .....*..... .....*..... .....*.....							475
HTPL-L	572	-----SSKSHE--AEQ--AVVKFFLNICYPFLLNPKVRVCVLLVYLVLVLAIAIYGCCTNMKEGLDPAKL							632
gi 1825729	469	-----SVPDEHGtdIH--PMSLFFRDYFGPFLTRSESKYFVFIYVLYIYIISSIIYGCYFHVQEGDLRNL							528
gi 1707052	451	-----HSASHD--VKQp-LTSRFFGEWYAPVLMHPVVRGIANVWFVYIYLLGASYGCSRIKEGLEPVL							522
gi 3892144	515	-----tssvstmsqtSPASKH--LHHC-AATSFERNWYAPVLMQPIRAIAGLWLYIYLGISIIYGCCTHLKEGLEPANL							592
gi 3892144	515	ipae fawkeqgspnsslSKSKD--REEKdrIVHFIGKIYGPFIILSNSVRIFSGLIFFVYLAIAIYGCYCNFREGLNPGNL							592
consensus	476	FLKDSPLVEYLRLREKHVWPYGLQVTVFVNPPDLTNPENRDRRLNEMVDEFENTPYAMGKNSTKFWLRDYENFLYSFISE							555
HTPL-L	633	ASDDSYITPYFNVEENYFSDYGPVRMIVITKVDYWDKDVQRKLENTKIFEKNVY-VDKNLTEFWLDAVYQYLK--GNS							709
gi 1825729	529	LVEDSYAIPHYRLLeKYFWKYQQQVQIVINNAPDLRNHTSRDRVHAMVLDFAATSKHAIGMESVQFWLFEMER-YYQKELE							607
gi 1707052	523	LVDDSYATPHYRVLeKHYWHYGASLQIVVSNPPDLRDPVERINMDKMASTFANCKKVAIGDDSVQFWLREMQ--VSEEIHK							600
gi 3892144	593	VTNDHYIAKYFSDI-KHFWRIGAQLHVAVLNPPNLTISENRNELLKVVSAFENTQYTLGREGTVFFLLEYLNLSELNAE							671
consensus	556	LEDEEEEFYDLEWFL-KSPGFSHWVGDLVWDN-KTDYETTIVKKFRFTTGKIDLSTWTDTRLLKTWRGVAD EYPDFN							633
HTPL-L	710	QDPNEKNTFMNNIPDFLSNFPNFQH-----DI-NISSSNEIISSRGF-IQTVDVSSSAKKILLFQLRRIA-EDCQIP							779
gi 1825729	608	VQIID-SSFYGLLHHFL-ASKTNNPLAEDIYWGpPDDDDNGTGVKSFRFILGMKDLVTTMDQTDATMSFREVAARWPEFN							685
gi 1707052	601	IQYDN-EKFYDHAQAQYI-YSDMSQPWVDVWVG--RNNNSERI IKTFRFMIGMRDISTTTKQTEATNTFREIASRFEQYN							676
gi 3892144	672	VEDTERLWKTKLNSWLK-YTGGS TQWASNLKIN-----KTDGSFQAFRFQIALKNFVEPNDKHAAQLLRDIADHQP-FN							744
consensus	634	VTVFDEDED-----AFFLDQILSIGPTTIQSIIWTLICMAVVCFLFIPNPNTVFVITVSI							686
HTPL-L	780	LMVYNQA-----FIYFDQYAAILEDVTRNVLVASAAMFIVSLLLIYPYPLCSLWVTFAI							832
gi 1825729	686	VTTFMPI-----WMFTDQYIIIIIPNTVQNII IALLVMIVIAVLFIPOQPMCSLWVALAC							738
gi 1707052	677	VTTYMPL-----WLFTDQYALVVPNTMQDIIIVACMLVISALLIIPQVCSFWAVTI							729
gi 3892144	745	VVYHEVsfgnrkilndfisshscyaqknipklaFPFADQYLIILPATIQNVVISLLCMAVVSFLLVPSLPSGFI							824

## FIG. 1B

### Patched motif (Continued)

```
consensus 687 ASIDIGVFGFLSLWGVLDLPISMITIIMSIGFSVDFSAHIAVHFYRSHGSETPDERLADALEALGWPVIOAALSTILCVL 766
HTPL-L      833 GSVIVGVTGFMAFWKVNLDISIMINLVICTGFSDFSAHISYAFV-SSSQPSVNQKSVEALYLLGYPVLQSAISTIGVC 911
gi 1825729 739 ASIDFGVIGYMTLWGVNLDASMITIIMSIGFSVDYSAHIAVGYVVSRED-TAAGR VKEALSALGWPLSQGAMSTIIAVS 817
gi 1707052 730 GSIDLGVLGFMTLWNVNLDASMITIIMSVGFSVDYSAHITVAYVISKES-TTSARVCDALGDLGWPVQAQGAMSTILAVS 808
gi 3892144 825 VSINIGVFGYMTLWGVNLDASVMSIIMSIGFAVDLSAHIIYAFVTSHG--DTKQRVIGALETLGWPIFQGASSTIAGIS 902

consensus 767 PLLFVPSYMVVVFCKTIFLVVIGLLHGLIFLPIILSLFVT-----IRTSNAKIKKPSSI 821
HTPL-L      912 VLAARAKAYIFRTFFKIMFLVMIPGAHGLIFIPVFLTFGRfi----- 954
gi 1825729 818 VLADIPAYMIVTFFKTVVLSISLGLHGLVFLPVLLSIFVRgcciipssphGHPSAQKIEKQIRI 882
gi 1707052 809 VLSDVPAYMIVTFFKTVFLAISIGFLHGLVFLPLMLSVFVGki-----fdIHISNISIKYCIYL 867
gi 3892144 903 ILYTVDAYIILVFFKTIWLTMLIGAIGHGLFFFIPIFLSLFPV-----EFFRIPKSSEL 954
```

Structure of the HTPL gene (Chr. 10p12.1 )

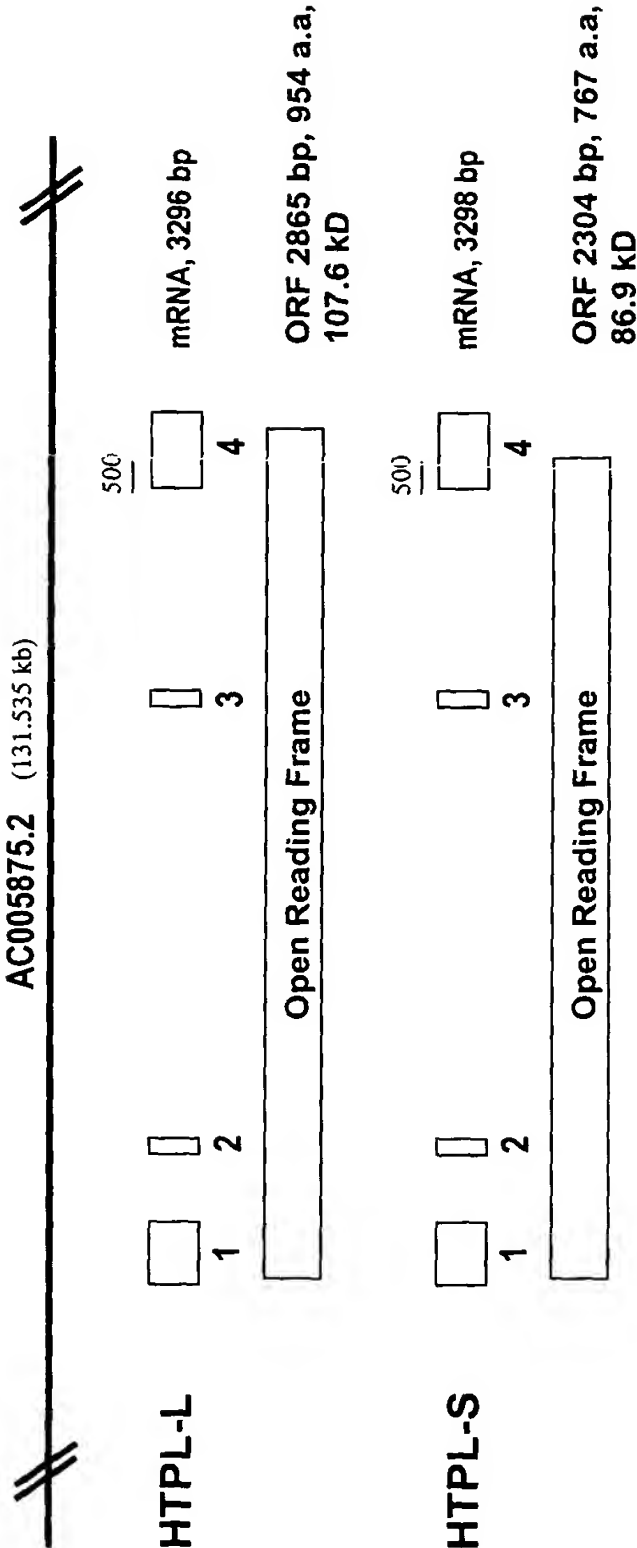


FIG. 2

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nt:  SEQ ID NO:  1
aa:  SEQ ID NO:  3
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FIG. 3

S	R	T	F	Q	W	L	G	W	Q	V	G	A	136
TCC	CGC	ACC	TTC	CAG	TGG	CTG	GGG	TGG	CAG	GTG	GGC	GCG	485
H	P	W	I	F	L	L	A	P	L	M	L	T	149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA	524
A	A	L	G	T	G	F	L	Y	L	P	K	D	162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC	563
E	E	E	D	L	E	E	H	Y	T	P	V	G	175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG	602
S	P	A	K	A	E	R	R	F	V	Q	G	H	188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTC	CAG	GGC	CAT	641
F	T	T	N	D	S	Y	R	F	S	A	S	R	201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG	680
R	S	T	E	A	N	F	V	S	L	L	V	V	214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC	719
S	Y	S	D	S	L	L	D	P	A	T	F	A	227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA	758
E	V	S	K	L	D	G	A	V	Q	D	L	R	240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC	797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q	253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG	836
V	C	A	R	Y	R	A	L	C	V	P	P	N	266
GTG	TGC	GCG	AGG	TAC	AGG	GCG	CTC	TGC	GTG	CCC	CCC	AAC	875
P	I	L	Y	A	W	Q	V	N	K	T	L	N	279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC	914
L	S	S	I	S	F	P	A	Y	N	H	G	R	292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG	953
H	P	L	Y	L	T	G	F	F	G	G	Y	I	305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC	992

FIG. 3

L	G	G	S	L	G	M	G	Q	L	L	L	R	318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG	1031
A	K	A	M	R	L	L	Y	Y	L	K	T	E	331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG	1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T	344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC	1109
H	L	L	D	Q	F	T	N	I	K	N	I	L	357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG	1148
A	L	K	K	I	E	V	V	H	F	T	S	L	370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT	1187
S	R	Q	L	E	F	E	A	T	S	V	T	V	383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG	1226
I	P	V	F	H	L	A	Y	I	L	I	I	L	396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG	1265
F	A	V	T	S	C	F	R	F	D	C	I	R	409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA	1304
N	K	M	C	V	A	A	F	G	V	I	S	A	422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT	1343
F	L	A	V	V	S	G	F	G	L	L	L	H	435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC	1382
I	G	V	P	F	V	I	I	V	A	N	S	P	448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTT	GCC	AAT	TCA	CCA	1421
F	L	I	L	G	V	G	V	D	D	M	F	I	461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC	1460
M	I	S	A	W	H	K	T	N	L	A	G	D	474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GGT	GAC	1499
I	R	E	R	M	S	N	V	Y	S	K	A	A	487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA	1538

FIG. 3



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V	S	I	T	I	T	T	I	T	N	I	L	A	500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC	1577
L	Y	T	G	I	M	S	S	F	R	S	V	Q	513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCC	GTA	CAA	1616
C	F	C	I	Y	T	G	T	T	L	L	F	C	526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ACG	ACC	CTG	TTA	TTT	TGC	1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A	539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC	1694
L	D	G	K	R	E	V	V	C	L	C	W	L	552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG	1733
K	K	A	D	P	K	W	P	S	F	K	K	F	565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC	1772
C	C	F	P	F	G	S	V	P	D	E	H	G	578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA	1811
T	D	I	H	P	M	S	L	F	F	R	D	Y	591
ACT	GAT	ATC	CAT	CCA	ATG	AGT	TTG	TTT	TTT	AGA	GAC	TAT	1850
F	G	P	F	L	T	R	S	E	S	K	Y	F	604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT	1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I	617
GTA	GTC	TTT	ATA	TAT	GTT	TTG	TAC	ATC	ATA	AGC	AGT	ATA	1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R	630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA	1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F	643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT	2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R	656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG	2045
V	M	V	I	V	T	K	K	V	D	Y	W	D	669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT	2084

FIG. 3

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K	D	V	R	Q	K	L	E	N	C	T	K	I	682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT	2123
F	E	K	N	V	Y	V	D	K	N	L	T	E	695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG	2162
F	W	L	D	A	Y	V	Q	Y	L	K	G	N	708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC	2201
S	Q	D	P	N	E	K	N	T	F	M	N	N	721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT	2240
I	P	D	F	L	S	N	F	P	N	F	Q	H	734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT	2279
D	I	N	I	S	S	S	N	E	I	I	S	S	747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC	2318
R	G	F	I	Q	T	T	D	V	S	S	S	A	760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC	2357
K	K	K	I	L	L	F	Q	L	R	R	I	A	773
AAA	AAG	AAA	ATA	TTG	TTA	TTC	CAA	TTA	CGA	CGC	ATA	GCT	2396
E	D	C	Q	I	P	L	M	V	Y	N	Q	A	786
GAA	GAC	TGT	CAA	ATT	CCC	CTA	ATG	GTG	TAT	AAC	CAG	GCA	2435
F	I	Y	F	D	Q	Y	A	A	I	L	E	D	799
TTT	ATA	TAT	TTT	GAT	CAG	TAT	GCT	GCA	ATA	TTA	GAA	GAC	2474
T	V	R	N	V	L	V	A	S	A	A	M	F	812
ACT	GTT	AGA	AAT	GTA	TTG	GTT	GCA	TCA	GCA	GCT	ATG	TTC	2513
I	V	S	L	L	L	I	P	Y	P	L	C	S	825
ATT	GTT	TCC	TTA	TTG	TTA	ATC	CCT	TAT	CCA	TTG	TGT	TCC	2552
L	W	V	T	F	A	I	G	S	V	I	V	G	838
TTG	TGG	GTG	ACT	TTT	GCT	ATC	GGT	TCT	GTG	ATT	GTA	GGG	2591
V	T	G	F	M	A	F	W	K	V	N	L	D	851
GTA	ACG	GGT	TTC	ATG	GCA	TTC	TGG	AAA	GTC	AAT	CTT	GAT	2630

FIG. 3

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S	I	S	M	I	N	L	V	I	C	T	G	F	864
TCC	ATA	TCC	ATG	ATT	AAT	CTT	GTC	ATT	TGT	ACA	GGG	TTT	2669
S	F	D	F	S	A	H	I	S	Y	A	F	V	877
TCT	TTC	GAT	TTT	TCT	GCA	CAC	ATT	TCC	TAT	GCA	TTT	GTT	2708
S	S	S	Q	P	S	V	N	Q	K	S	V	E	890
TCT	AGT	TCT	CAA	CCC	TCA	GTA	AAC	CAA	AAA	TCA	GTT	GAG	2747
A	L	Y	L	L	G	Y	P	V	L	Q	S	A	903
GCA	TTG	TAT	CTT	CTA	GGC	TAC	CCA	GTG	TTA	CAA	AGT	GCA	2786
I	S	T	I	I	G	V	C	V	L	A	A	A	916
ATT	TCA	ACA	ATA	ATA	GGG	GTG	TGT	GTT	TTA	GCT	GCA	GCG	2825
K	A	Y	I	F	R	T	F	F	K	I	M	F	929
AAA	GCA	TAC	ATC	TTC	AGA	ACA	TTT	TTT	AAG	ATT	ATG	TTT	2864
L	V	M	I	F	G	A	A	H	G	L	I	F	942
CTT	GTT	ATG	ATA	TTT	GGG	GCA	GCT	CAT	GGC	CTA	ATT	TTT	2903
I	P	V	F	L	T	F	F	G	R	F	I	*	955
ATT	CCA	GTA	TTC	TTA	ACC	TTT	TTT	GGA	AGG	TTT	ATT	TGA	2942
ATATCCACTAACAAGTCAAAGACCAATTCTAGAATTCCTGATTGCCCTATTC													2994
CAATCTGATTTTTTTTAAATGCACTATTAAGAATAGTCAACAAACTACTGGGA													3046
GGCCAAAGTGGGTGGATCACCTGAGGTCAAGAATTCGAGACCAGCCTGGCCA													3098
ACATGGTGAAACCTCGACACTACTGAAAATACAAAAATTATCCAGGCATGGT													3150
GGCGTGACCTATAATCCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCT													3202
TGAACCTGGGAGATGGAGGTTGCAGTGAGCTGGAGTGCACCAGGCACTCCAG													3254
CCTGGGTGACAAGAATGAGACTCCGTCTCAGAAAAAAAAAAAA													3296

FIG. 3

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## HTPL-S

nt: SEQ ID NO: 4  
aa: SEQ ID NO: 6

CAGGAAACCGTCTGGTGGGATCTCCGCAGCTGCTTTTCACCTGCTGTTCCCTC	52
	M P W V E P 6
CTGCGCTTCCTAAGAGGAAGAATCA ATG CCG TGG GTG GAG CCC	95
K P R P G P E Q K P K L T	19
AAG CCC AGG CCG GGG CCG GAG CAG AAG CCC AAG CTC ACC	134
K P D S A T G P Q W Y Q E	32
AAA CCG GAC TCT GCC ACC GGG CCG CAG TGG TAC CAG GAA	173
S Q E S E S E G K Q P P P	45
TCT CAG GAA TCG GAG TCG GAA GGC AAG CAG CCA CCC CCG	212
G P L A P P K S P E P S G	58
GGA CCC CTG GCA CCC CCG AAA TCC CCC GAA CCC TCA GGA	251
P L A S E Q D A P L P E G	71
CCC CTG GCG TCG GAG CAG GAT GCA CCC CTG CCA GAG GGG	290
D D A P P R P S M L D D A	84
GAC GAT GCA CCC CCC CCG CCG TCG ATG CTG GAC GAT GCA	329
P R L P L E L D D A P L P	97
CCC CGC CTG CCG CTG GAG CTG GAC GAT GCA CCC CTG CCG	368
E E E T P E P T A I C R H	110
GAG GAG GAA ACC CCC GAA CCC ACG GCC ATC TGC AGG CAC	407
R H R C H T D C L E G L L	123
CGG CAC CGC TGT CAC ACC GAC TGC CTA GAG GGG CTG CTG	446
S R T F Q W L G W Q V G A	136
TCC CGC ACC TTC CAG TGG CTG GGG TGG CAG GTG GGC GCG	485

FIG. 4

H	P	W	I	F	L	L	A	P	L	M	L	T	149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA	524
A	A	L	G	T	G	F	L	Y	L	P	K	D	162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC	563
E	E	E	D	L	E	E	H	Y	T	P	V	G	175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG	602
S	P	A	K	A	E	R	R	F	V	Q	G	H	188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTG	CAG	GGC	CAT	641
F	T	T	N	D	S	Y	R	F	S	A	S	R	201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG	680
R	S	T	E	A	N	F	V	S	L	L	V	V	214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC	719
S	Y	S	D	S	L	L	D	P	A	T	F	A	227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA	758
E	V	S	K	L	D	G	A	V	Q	D	L	R	240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC	797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q	253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG	836
V	C	A	R	Y	R	A	L	C	V	P	P	N	266
GTG	TGC	GCG	AGG	TAC	AGG	GCG	CTC	TGC	GTG	CCC	CCC	AAC	875
P	I	L	Y	A	W	Q	V	N	K	T	L	N	279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC	914
L	S	S	I	S	F	P	A	Y	N	H	G	R	292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG	953
H	P	L	Y	L	T	G	F	F	G	G	Y	I	305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC	992
L	G	G	S	L	G	M	G	Q	L	L	L	R	318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG	1031

FIG. 4

A	K	A	M	R	L	L	Y	Y	L	K	T	E	331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG	1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T	344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC	1109
H	L	L	D	Q	F	T	N	I	K	N	I	L	357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG	1148
A	L	K	K	I	E	V	V	H	F	T	S	L	370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT	1187
S	R	Q	L	E	F	E	A	T	S	V	T	V	383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG	1226
I	P	V	F	H	L	A	Y	I	L	I	I	L	396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG	1265
F	A	V	T	S	C	F	R	F	D	C	I	R	409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA	1304
N	K	M	C	V	A	A	F	G	V	I	S	A	422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT	1343
F	L	A	V	V	S	G	F	G	L	L	L	H	435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC	1382
I	G	V	P	F	V	I	I	V	A	N	S	P	448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTT	GCC	AAT	TCA	CCA	1421
F	L	I	L	G	V	G	V	D	D	M	F	I	461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC	1460
M	I	S	A	W	H	K	T	N	L	A	D	D	474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GAT	GAC	1499
I	R	E	R	M	S	N	V	Y	S	K	A	A	487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA	1538
V	S	I	T	I	T	T	I	T	N	I	L	A	500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC	1577

FIG. 4

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L	Y	T	G	I	M	S	S	F	R	S	V	Q	513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCT	GTA	CAA	1616
C	F	C	I	Y	T	G	M	T	L	L	F	C	526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ATG	ACC	CTG	TTA	TTT	TGC	1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A	539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC	1694
L	D	G	K	R	E	V	V	C	L	C	W	L	552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG	1733
K	K	A	D	P	K	W	P	S	F	K	K	F	565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC	1772
C	C	F	P	F	G	S	V	P	D	E	H	G	578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA	1811
T	D	I	H	P	I	S	L	F	F	R	D	Y	591
ACT	GAT	ATC	CAT	CCA	ATA	AGT	TTG	TTT	TTT	AGA	GAC	TAT	1850
F	G	P	F	L	T	R	S	E	S	K	Y	F	604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT	1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I	617
GTA	GTC	TTT	ATA	TAT	GTT	TTG	TAC	ATC	ATA	AGC	AGT	ATA	1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R	630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA	1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F	643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT	2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R	656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG	2045
V	M	V	I	V	T	K	K	V	D	Y	W	D	669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT	2084
K	D	V	R	Q	K	L	E	N	C	T	K	I	682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT	2123
F	E	K	N	V	Y	V	D	K	N	L	T	E	695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG	2162

FIG. 4

F	W	L	D	A	Y	V	Q	Y	L	K	G	N	708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC	2201
S	Q	D	P	N	E	K	N	T	F	M	N	N	721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT	2240
I	P	D	F	L	S	N	F	P	N	F	Q	H	734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT	2279
D	I	N	I	S	S	S	N	E	I	I	S	S	747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC	2318
R	G	F	I	Q	T	T	D	V	S	S	S	A	760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC	2357
K	K	K	I	L	L	F	*						768
AAA	AAG	AAA	ATA	TTG	TTA	TTC	TAA	TTACGACGCATAGCTGAAG					2400
ACTGTCAAATTCCCCTAATGGTGTATAACCAGGCATTTATATATTTTGATCA													2452
GTATGCTGCAATATTAGAAGACACTGTTAGAAATGTATTGGTTGCATCAGCA													2504
GCTATGTTTCATTGTTTCCTTATTGTTAATCCCTTATCCATTGTGTTCCTTGT													2556
GGGTGACTTTTGCTATTGGTTCTGTGATTGTAGGGGTAACGGGTTTCATGGC													2608
ATTCTGGAAAGTCAATCTTGATTCCATATCCATGATTAATCTTGTCAATTTGT													2660
ATAGGGTTTTCTTTTCGATTTTTCTGTACACATTTCCCTATGCATTTGTTTCTA													2712
GTTCTCAACCCTCAGTAAACCAAAAATCAGTTGAGGCATTGTATCTTCTAGG													2764
CTACCCAGTGTTACAAAGTGCAATTTCAACAATAATAGGGGTGTGTGTTTTA													2816
GCTGCAGCGAAAGCATACATCTTCAGAACATTTTTTAAGATTATGTTTCTTG													2868
TTATGATATTTGGGGCAGCTCATGGCCTAATTTTTATTCCAGTATTCTTAAC													2920
CTTTTTTGGAAGGTTTATTTGAATATCCACTAACAAGTCAAAGACCAATTCT													2972
AGAATTCCTGATTGCCCTATTCCAATCTGATTTTTTTAAATGCACTATTAAG													3024
AATAGTCAACAACTACTGGGAGGCCAAGGTGGGTGGATCACCTGAGGTCAA													3076

FIG. 4



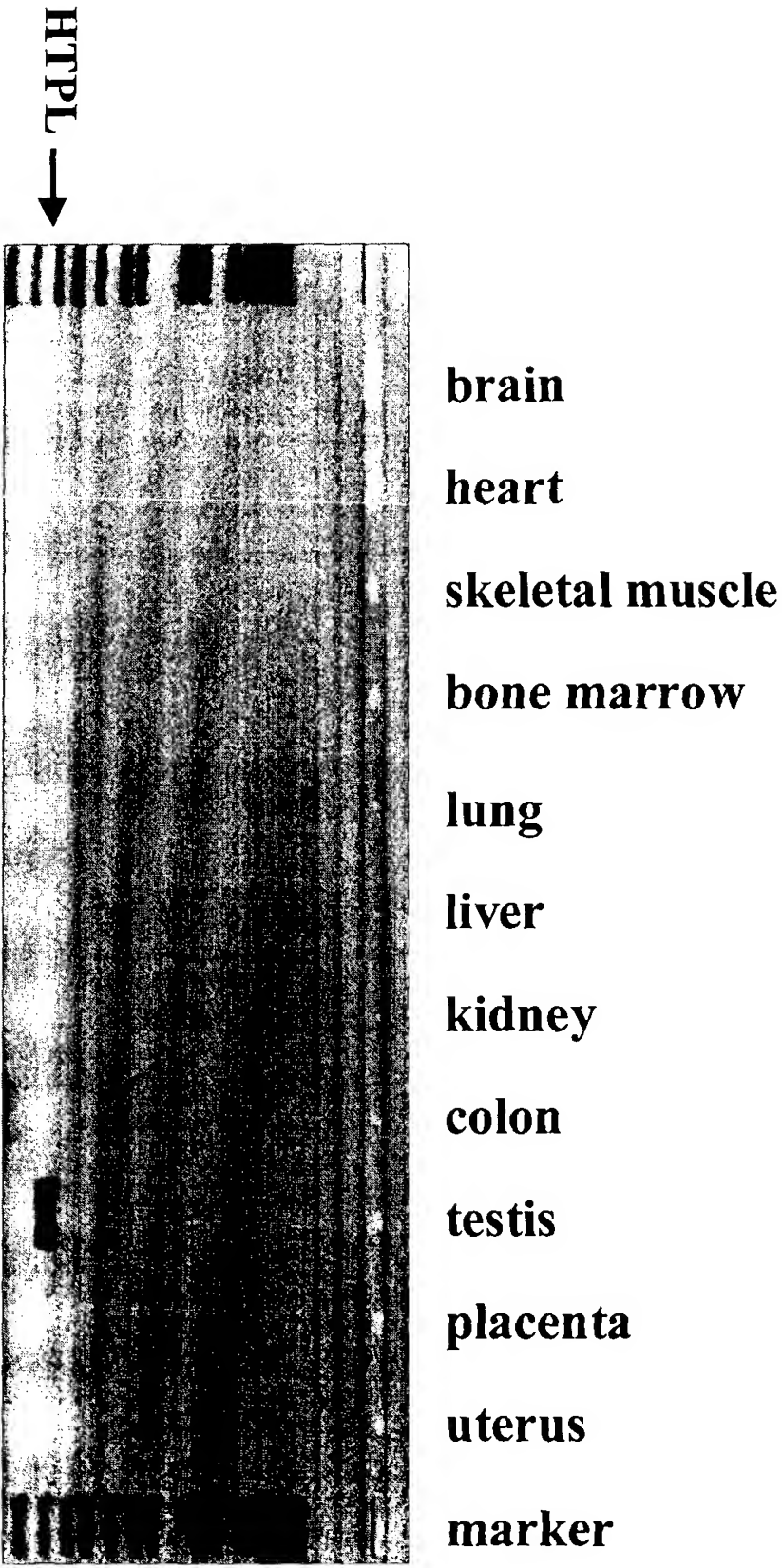
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GAATTCGAGACCAGCCTGGCCAACATGGTGAAACCTCGACACTACTGAAAAT	3128
ACAAAAATTATCCAGGCATGGTGGCGTGCACCTATAATCCCAGCTACCTGGG	3180
AGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGATGGAGGTTGCAGTGAGC	3232
TGGAGTGCACCAGGCACTCCAGCCTGGGTGACAAGAATGAGACTCCGTCTCA	3284
GAAAAAAAAAAAAA	3298

GAATTCGAGACCAGCCTGGCCAACATGGTGAAACCTCGACACTACTGAAAAT  
ACAAAAATTATCCAGGCATGGTGGCGTGCACCTATAATCCCAGCTACCTGGG  
AGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGATGGAGGTTGCAGTGAGC  
TGGAGTGCACCAGGCACTCCAGCCTGGGTGACAAGAATGAGACTCCGTCTCA  
GAAAAAAAAAAAAA

FIG. 4

**HTPL tissue distribution by RT-PCR**



**FIG. 5**

50660736 or 543066